

# biclust - A Toolbox for Bicluster Analysis in **R**

**Sebastian Kaiser and Friedrich Leisch**

Institut für Statistik  
Ludwig-Maximilians-Universität München

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# **Overview**

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## **Outline:**

**Introduce Biclustering**

**The biclust - Package**

**Examples**

**Future Work**

# Biclustering

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## Why Biclustering?

- Simultaneous clustering of 2 dimensions
- Large datasets where clustering leads to diffuse results
- Only parts of the data influence each other

# Biclustering

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**Initial Situation:**

**Two-Way Dataset**

	$c_1$	$\dots$	$c_i$	$\dots$	$c_m$
$r_1$	$a_{11}$	$\dots$	$a_{i1}$	$\dots$	$a_{m1}$
$\vdots$	$\vdots$	$\ddots$	$\vdots$	$\ddots$	$\vdots$
$r_j$	$a_{1j}$	$\dots$	$a_{ij}$	$\dots$	$a_{mj}$
$\vdots$	$\vdots$	$\ddots$	$\vdots$	$\ddots$	$\vdots$
$r_n$	$a_{1n}$	$\dots$	$a_{in}$	$\dots$	$a_{mn}$

# Biclustering

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## Goal:

Finding subgroups of rows and columns which are as similar as possible to each other and as different as possible to the rest.

The diagram illustrates the goal of biclustering. On the left, there is a 7x7 matrix with elements represented by 'A' or '\*'. The matrix is:

A	*	*	A	*	A	*
*	*	*	*	*	*	*
*	*	*	*	*	*	*
A	*	*	A	*	A	*
*	*	*	*	*	*	*
A	*	*	A	*	A	*
*	*	*	*	*	*	*

An arrow points from the left matrix to the right, indicating the transformation. On the right, there is a 4x4 matrix divided into four quadrants by a vertical and horizontal line through the center. The top-left quadrant contains three 'A's. The other three quadrants contain only '\*' symbols. This represents a 2x2 clustering of the original matrix into four subgroups.

A	A	A	*	*	*	*
A	A	A	*	*	*	*
A	A	A	*	*	*	*
*	*	*	*	*	*	*
*	*	*	*	*	*	*
*	*	*	*	*	*	*
*	*	*	*	*	*	*

# More than one bicluster?

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Most Bicluster Algorithms are iterative. To find the next bicluster given  $n-1$  found bicluster you have to either

- ignore the  $n-1$  already found bicluster,
- delete rows and/or columns of the found bicluster or
- mask the found bicluster with random values.

# The biclust - Package - Algorithms

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Chosen sample of algorithms in order to cover most bicluster outcomes.

**Bimax(Barkow et al. (2006)):** Groups with ones in binary matrix

**CC (Cheng and Church (2000)):** Constant values

**Plaid (Turner et al. (2005)):** Constant values over rows or columns

**Spectral (Kluger et al. (2003)):** Coherent values over rows and columns

**Xmotifs (Murali and Kasif (2003)):** Coherent correlation over rows and columns

# The biclust - Package

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## Function: biclust

The main function of the package is

```
biclust(data,method=BCxxx(),number,...)
```

with:

**data:** The preprocessed data matrix

**method:** The algorithm used (E. g. BCCC() for CC)

**number:** The maximum number of bicluster to search for

**... :** Additional parameters of the algorithms

Returns an object of class Biclust for uniform treatment.

# The biclust - Package

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## Additional methods

**Preprocessing:** `discretize()`, `binarize()`, ...

**Visualization:** `parallelCoordinates()`, `drawHeatmap()`, `Bubbleplot()`

**Validation:** `jaccardind()`, `clusterVariance()`, ...

# Validation: Jaccard

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## Jaccard index for biclustering

- Compare two bicluster results ( $Biclust1, Biclust2$ ).
- Percentage of datapoints in the same cluster.
- Only datapoints who are clustered in at least one of the results.
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$$JacInd(Biclust1, Biclust2) = \frac{|B1CP \cap B2CP|}{|B1CP| + |B2CP| - |B1CP \cap B2CP|}$$

- where  $BICP$  are the point combinations in a cluster in result  $BiclustI$

# Example

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## BicatYeast

- Subsample of the *Saccharomyces Cerevisiae* organism (Yeast)
- Used to present bicluster algorithms by Barkow et al. (2006)
- Microarray data: 419 genes, 80 experiments

## Example: BicatYeast

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```
> data(BicatYeast)
> x<-discretize(BicatYeast)
> Xmotif<-biclust(x, method=BCXmotifs(), number=50, alpha=0.05,
+ nd=20, ns=20, sd=5)
> Xmotif
```

An object of class Biclust

call:

```
biclust(x = x, method = BCXmotifs(), number = 50, alpha = 0.05)
```

Number of Clusters found: 15

First Cluster size:

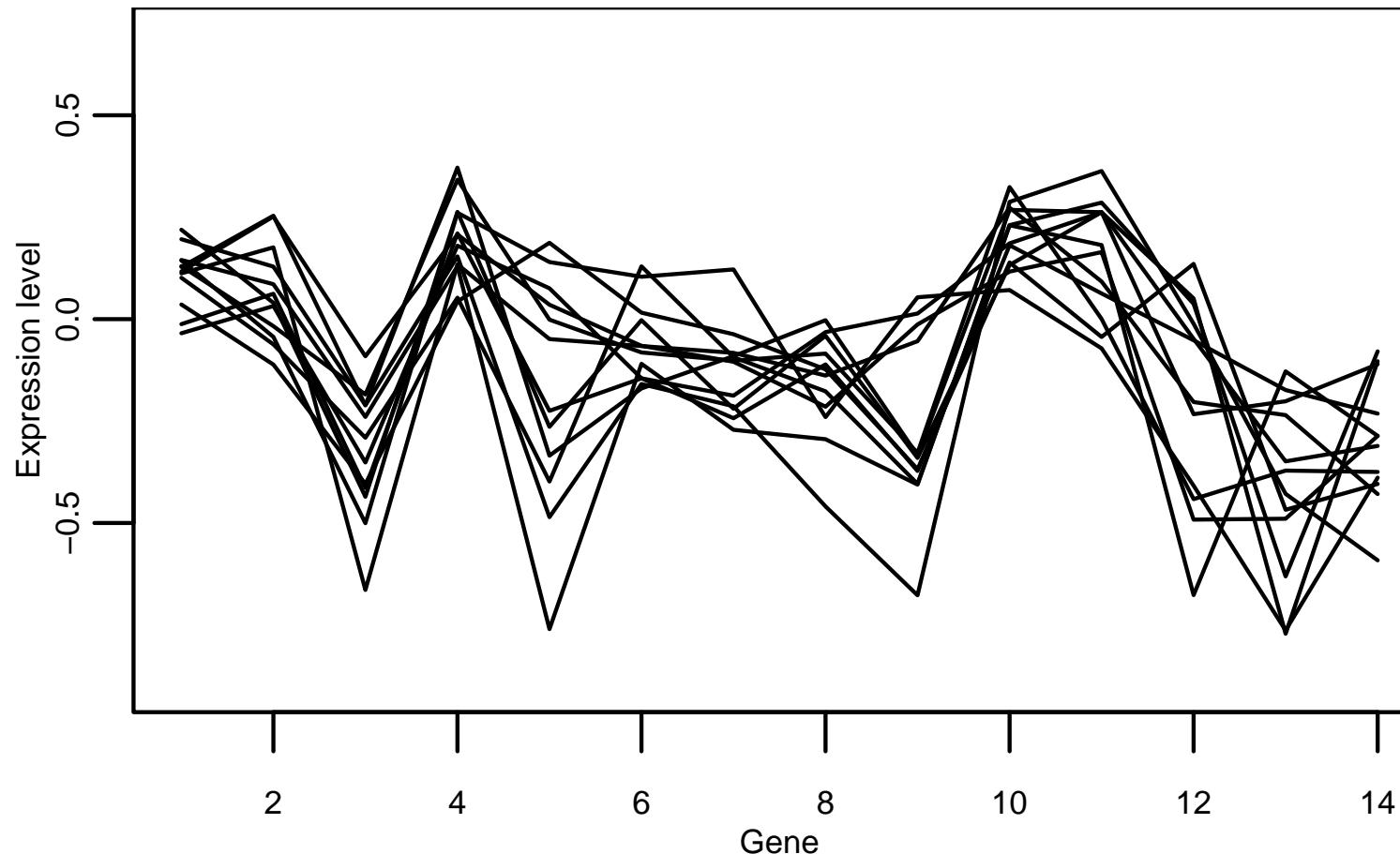
Number of Rows: 175

Number of Columns: 6

## Example: BicatYeast

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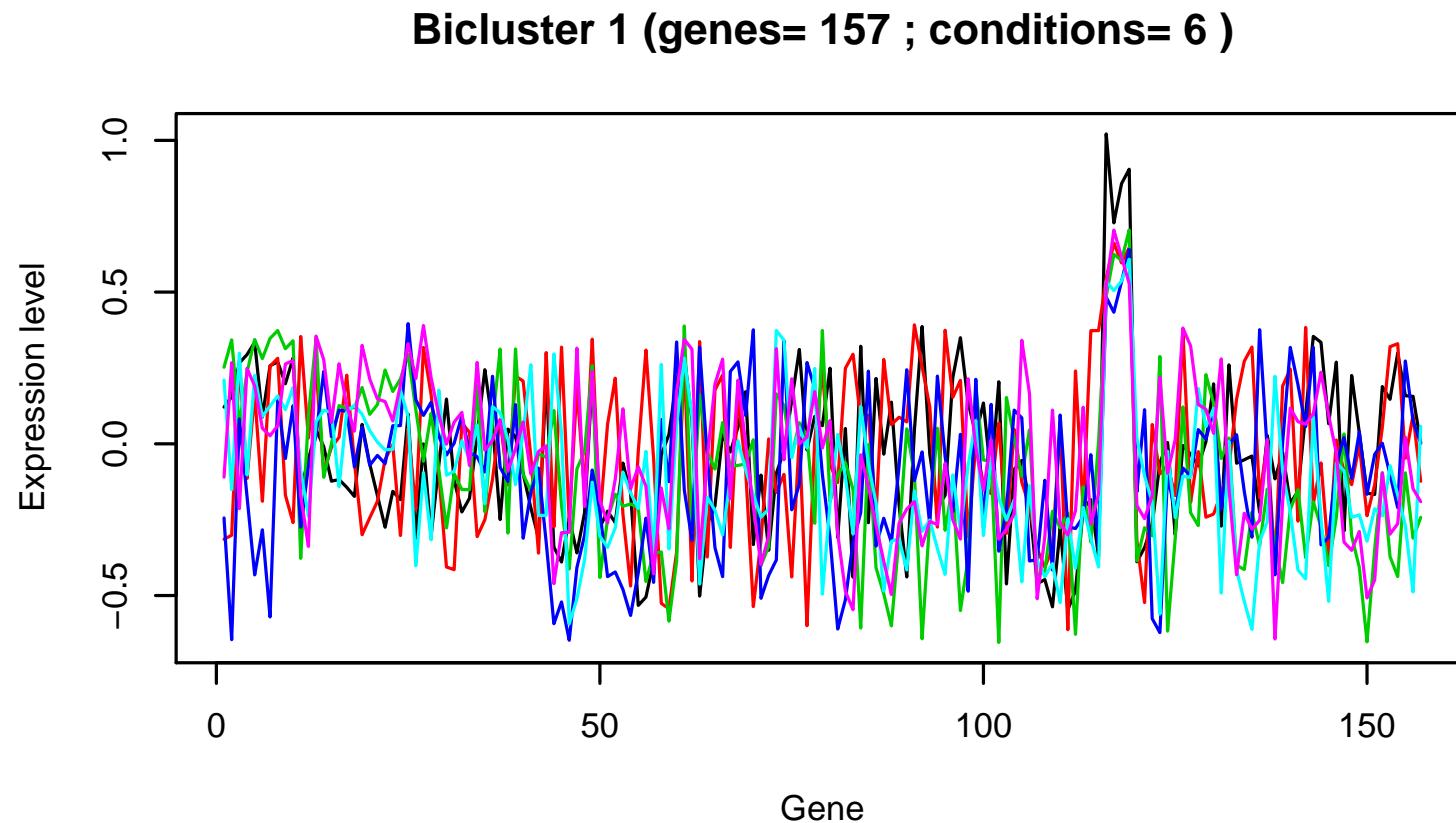
```
> parallelCoordinates(x=BicatYeast, bicResult=Xmotif, number=6)
```



## Example: BicatYeast

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```
> parallelCoordinates(x=BicatYeast, bicResult=Xmotif, number=1,  
+ geneTitle=TRUE)
```



## Example: BicatYeast

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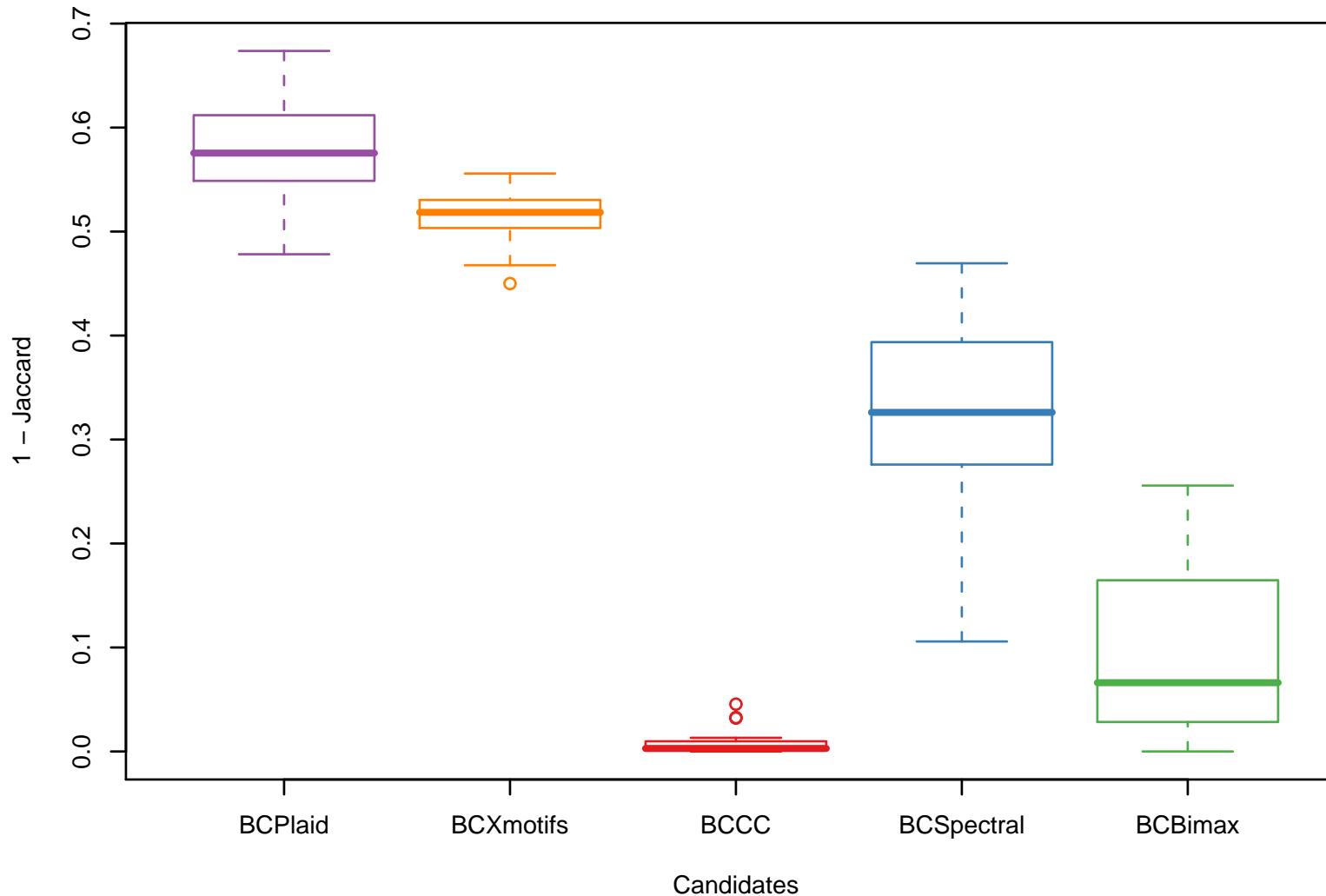
Jaccard index of the five algorithms on BicatYeast result

	BCPlaid	BCXmotifs	BCCC	BCSpect.	BCBimax
BCPlaid	1.0000	0.0007	0.0116	0.0000	0.0000
BCXmotifs	0.0007	1.0000	0.1789	0.0935	0.0000
BCCC	0.0116	0.1789	1.0000	0.0898	0.0036
BCSpectral	0.0000	0.0935	0.0898	1.0000	0.0000
BCBimax	0.0000	0.0000	0.0036	0.0000	1.0000

# Example: BicatYeast (Jaccard)

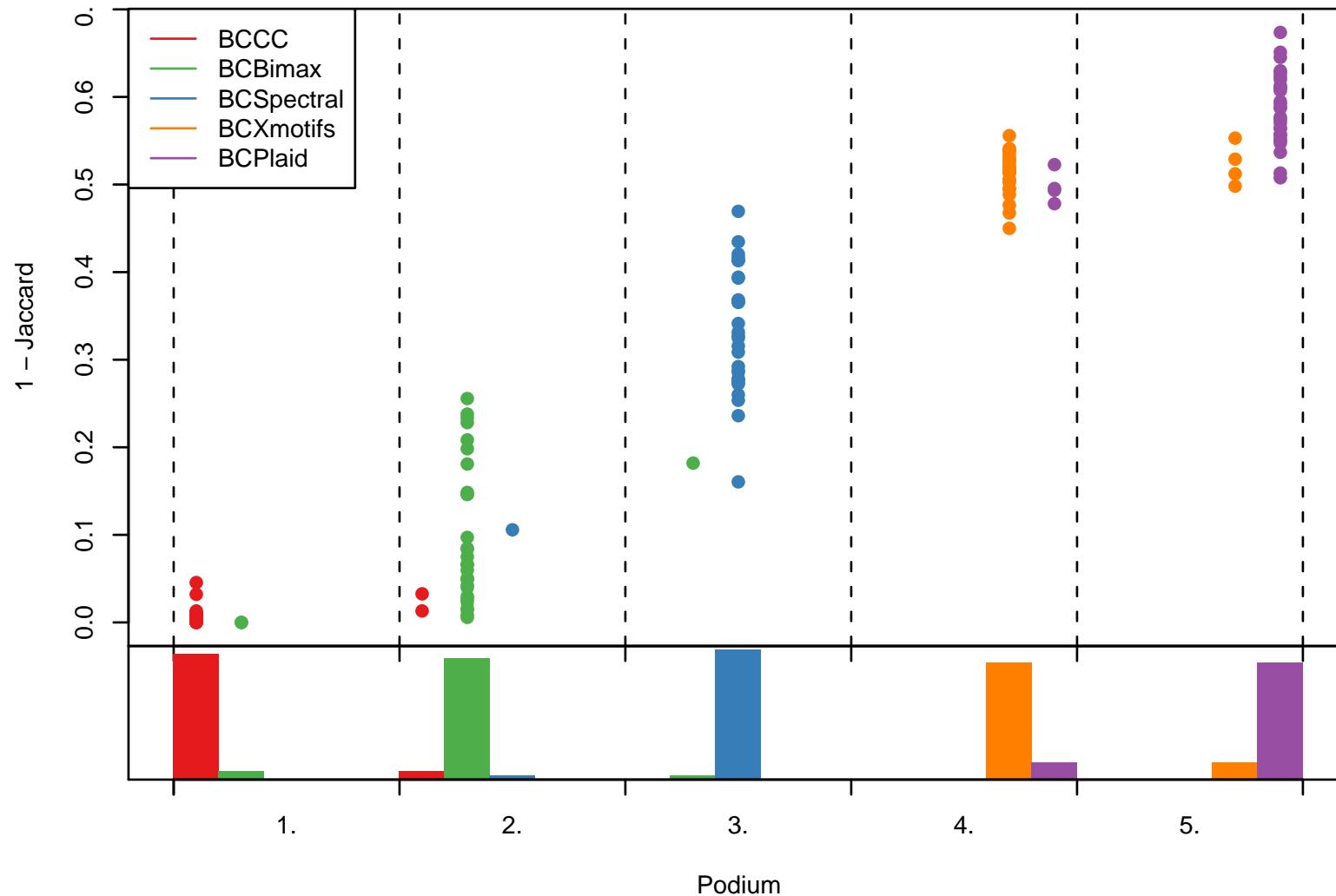
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## Adapted Jaccard Index (Boxplot)



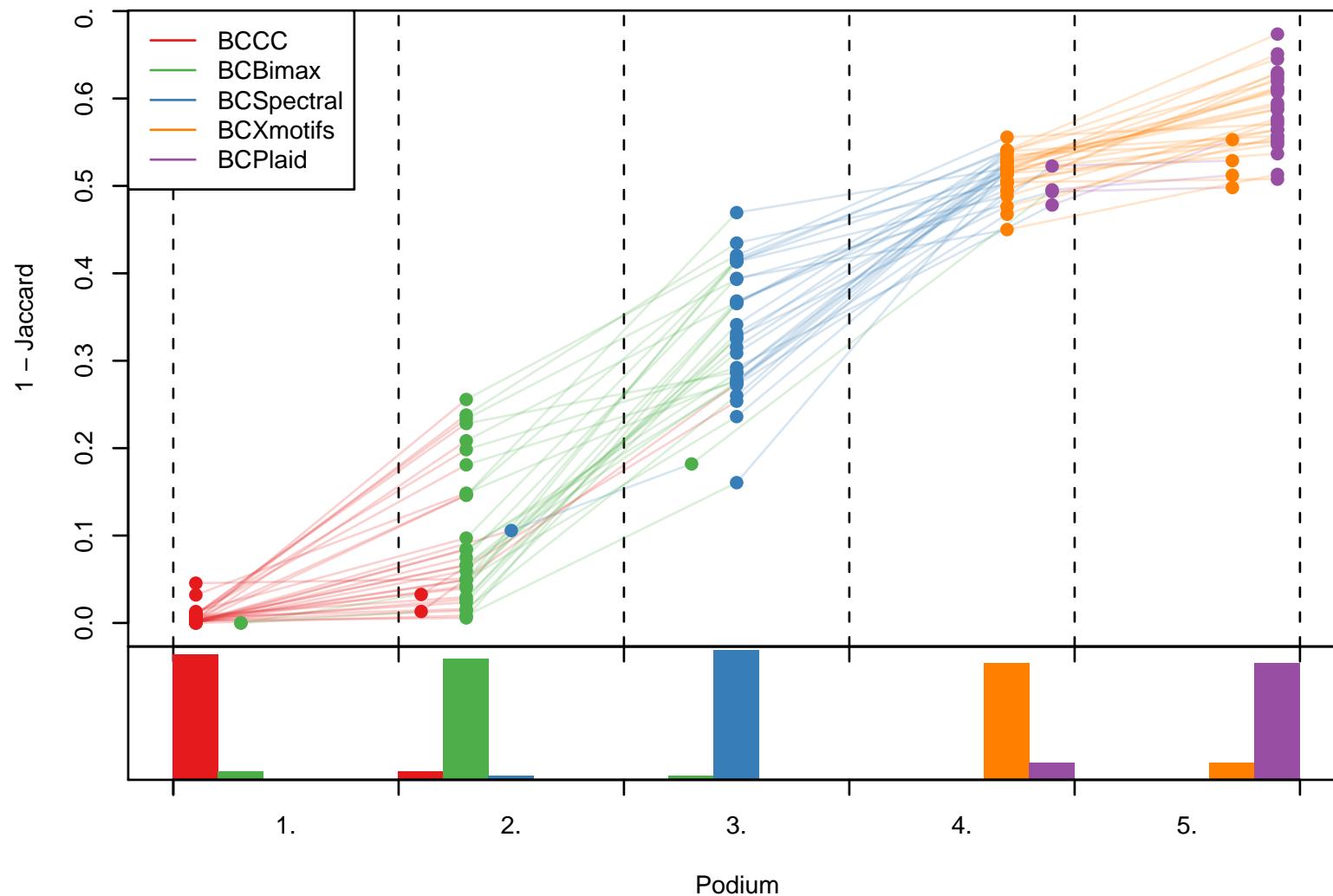
# Example: BiCatYeast (Jaccard)

## Adapted Jaccard Index (Beplot I)



# Example: BiCatYeast (Jaccard)

## Adapted Jaccard Index (Beplot II)



# Example

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## Australian Tourism Survey

- Survey of the Faculty of Commerce, University of Wollongong
- Questions on activities during the holidays
- 1003 people, 56 question blocks a about 15 questions
- Using a sample of 2 blocks (30 questions)

# Example: Tourism Data

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```
> x<-AUSTourismsurvey  
> Xmotif<-biclust(x, method=BCXmotifs(), number=10, alpha=0.05,  
+ ns=50, nd=50, sd=5)  
> Xmotif
```

An object of class `Biclust`

call:

```
biclust(x, method=BCXmotifs(), number=10, alpha=0.05)
```

Number of Clusters found: 7

First Cluster size:

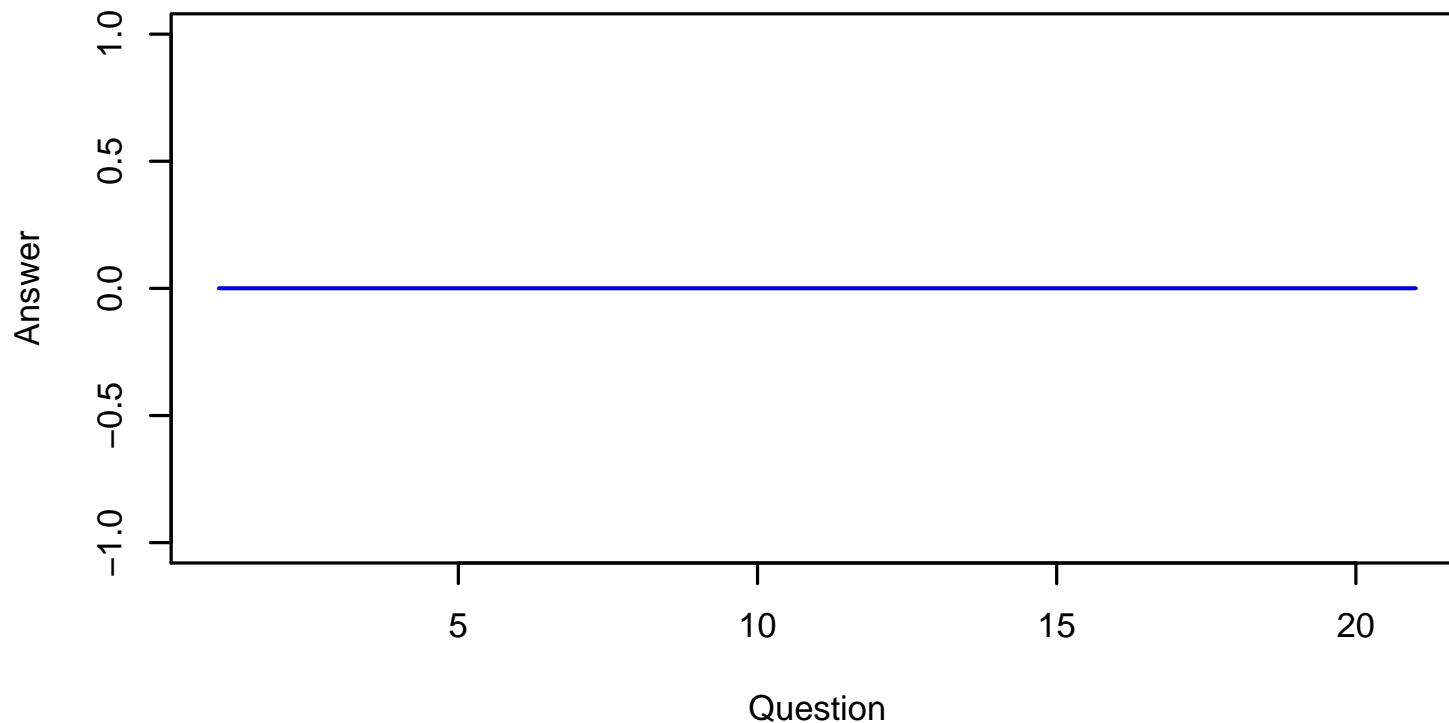
Number of Rows: 218

Number of Columns: 20

## Example: Tourism Data

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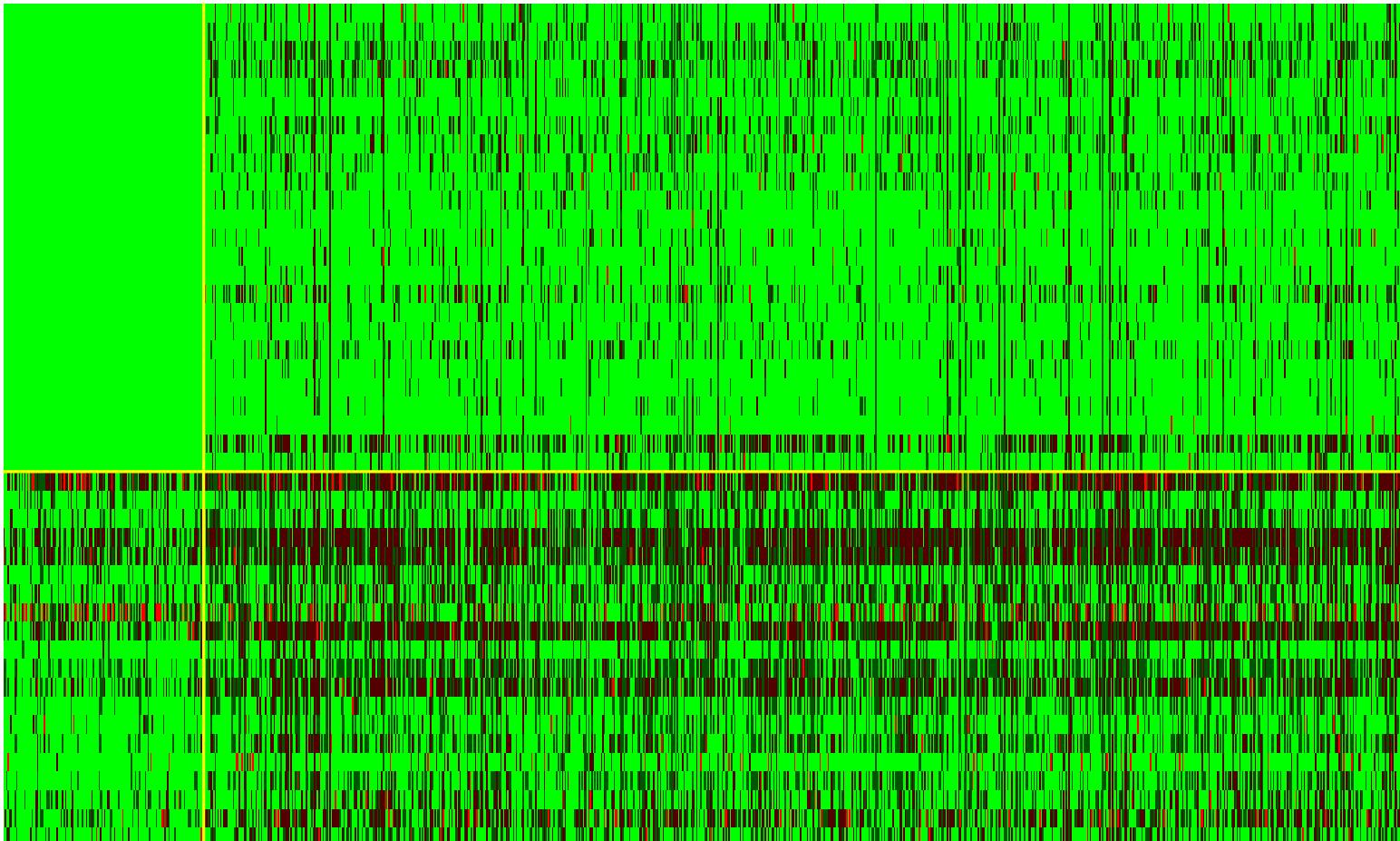
```
> parallelCoordinates( x=AUSTourismsurvey, bicResult=Xmotif, bicluster=1)
```



## Example: Tourism Data

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```
> drawHeatmap( x=AUSTourismsurvey, bicResult=Xmotif, bicluster=1)
```



# Future Work

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- Benchmark algorithms on more difficult scenarios.
- Compare algorithms in different application fields.
- Develop rules to choose bicluster algorithm.
- Develop a model based bicluster algorithm.
- Statistical tests on bicluster results.

# Acknowledgments

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The package `biclust` is a joint work with Microarray Analysis and Visualization Effort, University of Salamanca, Spain, especially Rodrigo Santamaria.

The `benchplot` is the work of Manuel Eugster, working group computational statistics, LMU Munich.

# References

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*biclust - A Toolbox for Bicluster Analysis in R*, Kaiser S. and Leisch F., Technical Report 28, Accepted for Compstat 2008-Proceedings in Computational Statistics.

See

<http://cran.r-project.org/package=biclust/> for the official release,

<http://r-forge.r-project.org/projects/biclust/> for the newest developments

and

<http://www.statistik.lmu.de/~kaiser/bicluster.html> for Papers and Links.